Assignment 5

Sharath Mudigoudr Shambu 2176980

Introduction

The analysis is about the individual has a diabetes or not which is done by conducting the full data analysis and the analysis of the survey on the basis of the data variables using different supervised and the non-supervised algorithms.

Summary

The Diabetes Prediction Dataset include patient medical and demographic information as well as the state of their diabetes (positive or negative). Features like age, gender, blood glucose level, smoking history, hypertension, heart disease, body mass index (BMI), and HbA1c level are among the features included in the data. Healthcare providers may find this helpful in identifying individuals who may be at risk of diabetes and in creating individualized treatment plans. Additionally, researchers can also utilize the dataset to investigate the associations between different demographic and medical characteristics and the risk of developing diabetes.The objective is to create three models for classification and clustering analysis, then assess each model's accuracy. Principal component analysis will also be used in the study to determine and examine the differences among the three categories.

Description of the experiment

I'm using the seven data mining approaches in this project. Data collection and integration, cleaning, preprocessing, clustering, classification, exploration, and evaluation. I'm utilizing ggplot for data visualization in order to determine the distributions of the variables. I'm viewing each numerical distribution as I analyze. Identifying the correlation between the variables, after which I use clustering (K Means) and classification (SVM and KKNN) in data mining approaches. To determine which model best fits the experiment and which technique yields the best accuracy. Lastly, I'm utilizing data evaluation to examine or display how well the multi-class classification task is doing. To evaluate the effectiveness of any classification model, I utilize ROC curve measurements.

1. Data gathering and integration
2. Data Exploration
3. Data Preprocessing
4. Clustering
5. Classification
6. Data Evaluation

The variables in the dataset are:

1. gender: Gender refers to the biological sex of the individual.
2. age: Age is an important factor as diabetes is more commonly diagnosed in older adults.Age ranges from 0-80 in our dataset.
3. hypertension: Hypertension is a medical condition in which the blood pressure in the arteries is persistently elevated.
4. heart_disease: Heart disease is another medical condition that is associated with an increased risk of developing diabetes.
5. smoking_history: Smoking history is also considered a risk factor for diabetes and can exacerbate the complications associated with diabetes.
6. bmi: BMI (Body Mass Index) is a measure of body fat based on weight and height.
7. HbA1c_level: HbA1c (Hemoglobin A1c) level is a measure of a person's average blood sugar level over the past 2-3 months.
8. blood_glucose_level: Blood glucose level refers to the amount of glucose in the bloodstream at a given time.
9. diabetes: Diabetes is the target variable being predicted, with values of 1 indicating the presence of diabetes and 0 indicating the absence of diabetes.

```
#Loading required libraries
library(ggplot2)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

library(factoextra)

## Warning: package 'factoextra' was built under R version 4.3.2

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa

library(ggfortify)

## Warning: package 'ggfortify' was built under R version 4.3.2

library(cluster)
library(caret)

## Loading required package: lattice

library(rpart)
library(e1071)
library(rattle)
```

```
## Loading required package: tibble

## Loading required package: bitops

## Rattle: A free graphical interface for data science with R.
## Version 5.5.1 Copyright (c) 2006-2021 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.

library(pROC)

## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

a. Data gathering and integration

The first part is to get the data you will use. You may use anything that has not been used in an assignment or tutorial. It must have at least 100 data points and must include both numerical and categorial (or ordinal) variables. I recommend keeping this relatively straightforward because data cleaning can take a lot of time if you choose a large, messy dataset. Kaggle (https://www.kaggle.com/datasets) and the University of California at Irvine (UCI) (https://archive.ics.uci.edu/ml/index.php) maintain collections of datasets, some even telling you if they are good examples for testing specific machine learning techniques. You may also choose to join together more than one dataset, for example to merge data on health outcomes by US state with a dataset on food statistics per state. Merging data is not required and will earn you a bonus point in this step.

```
diabetesDataSet <- read.csv("C:/Users/Dell/OneDrive/Desktop/DePaul/Fundamentals of
DS/Homeworks/diabetes_prediction_dataset.csv")
head(diabetesDataSet)

##   gender age hypertension heart_disease smoking_history   bmi HbA1c_level
## 1 Female  80           0             1           never 25.19         6.6
## 2 Female  54           0             0        No Info 27.32         6.6
## 3   Male  28           0             0           never 27.32         5.7
## 4 Female  36           0             0         current 23.45         5.0
## 5   Male  76           1             1         current 20.14         4.8
## 6 Female  20           0             0           never 27.32         6.6
##   blood_glucose_level diabetes
## 1                 140        0
## 2                  80        0
## 3                 158        0
## 4                 155        0
## 5                 155        0
## 6                  85        0
```

b. Data Exploration

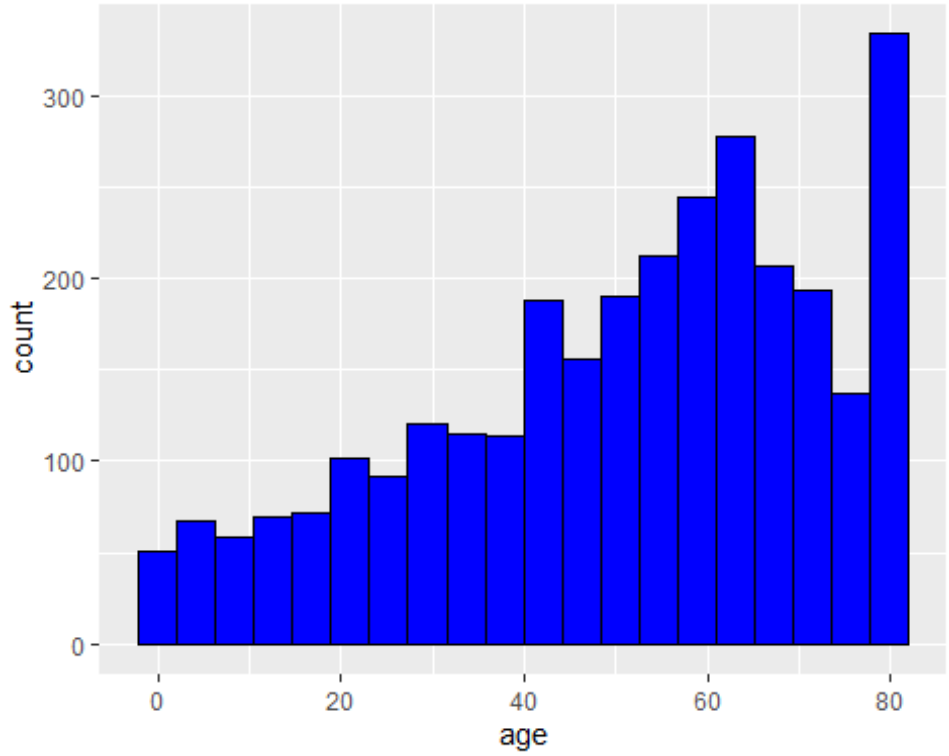
Using data exploration to understand what is happening is important throughout the pipeline, and is not limited to this step. However, it is important to use some exploration early on to make sure you understand your data. You must at least consider the distributions of each variable and at least some of the relationships between pairs of variables.

```
#Dimension of the data
dim(diabetesDataSet)

## [1] 100000      9
```

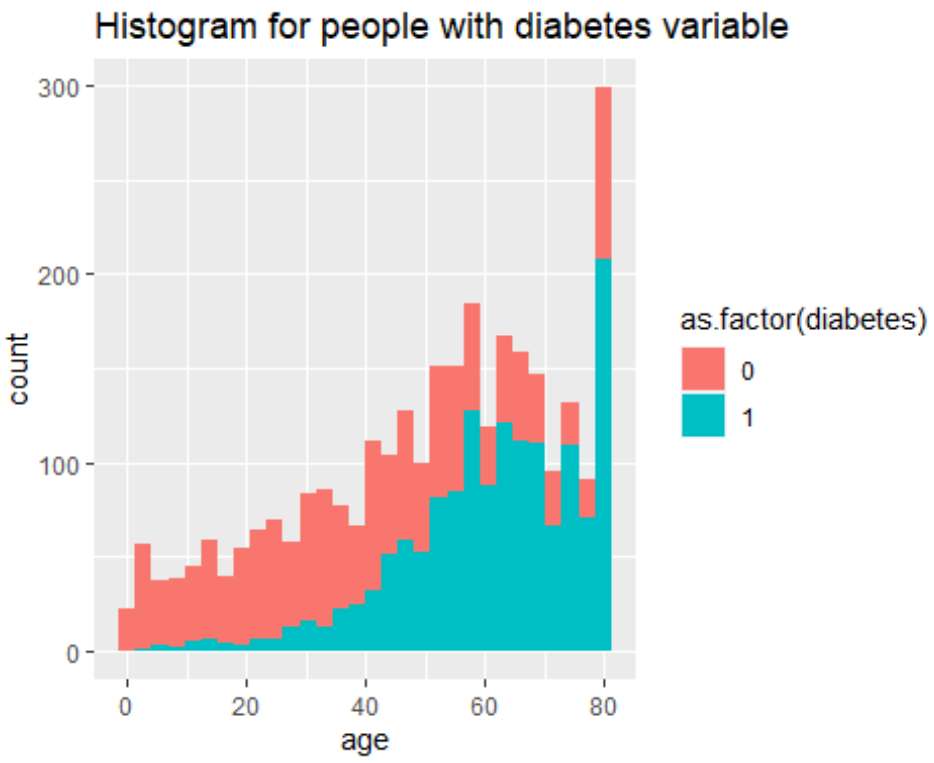
As this data is too large, as it has 100k observations. So I am taking only 3000 observations as a sample amount of data for doing analysis. Where data contains 1500 observations of people having diabetes and people don't have diabetes each.

```
diabetesData <-
  rbind(diabetesDataSet[diabetesDataSet$diabetes ==
0,][sample(1:nrow(diabetesDataSet[diabetesDataSet$diabetes == 0, ]), 1500),],
diabetesDataSet[diabetesDataSet$diabetes ==
1,][sample(1:nrow(diabetesDataSet[diabetesDataSet$diabetes == 1, ]), 1500),])

#Shuffling the Data
diabetesData <- diabetesData[sample(nrow(diabetesData)), ]

#Dimension of the data set
dim(diabetesData)

## [1] 3000    9

head(diabetesData)

##       gender age hypertension heart_disease smoking_history   bmi HbA1c_level
## 99151 Female  66           0             0          never 36.62         6.6
## 42865 Female  79           1             0          never 29.05         6.8
## 2691  Female  32           0             0       No Info 30.86         6.5
## 69981 Female  51           0             0          never 27.32         4.0
## 96893 Female  14           0             0       No Info 18.43         6.5
## 83729 Female  60           0             0          never 25.50         6.1
##       blood_glucose_level diabetes
## 99151                 155        1
## 42865                 155        1
## 2691                  100        0
## 69981                  90        0
## 96893                 159        1
## 83729                  90        0

#Visualizing the data for variable age
summary(diabetesData$age)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.16   36.00   54.00   50.61   68.00   80.00
```

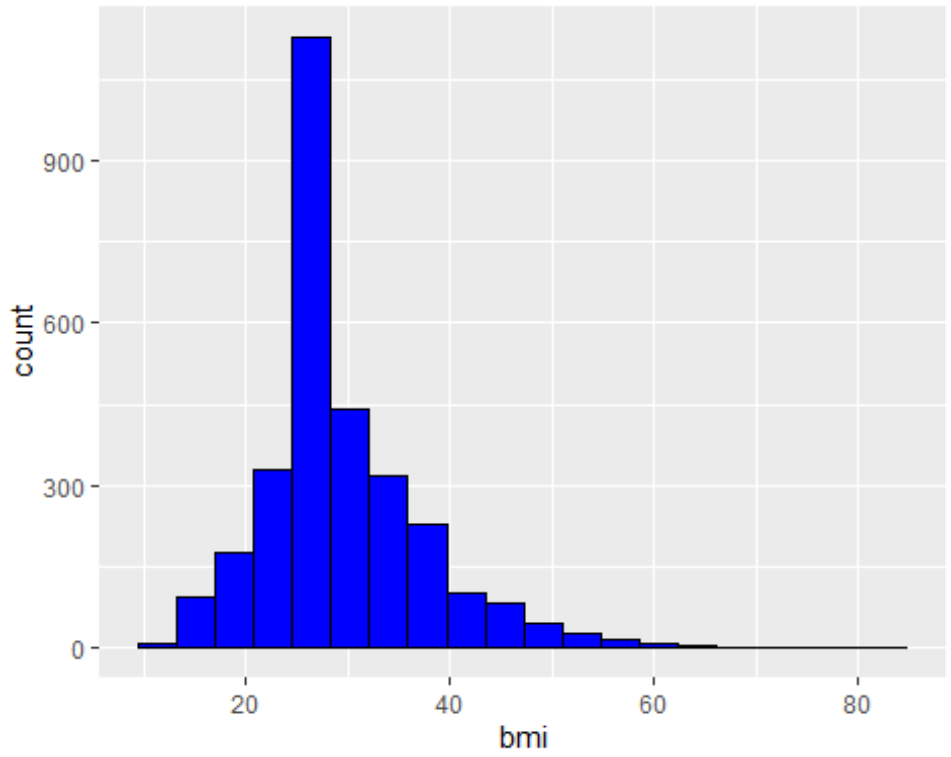
```
ggplot(diabetesData, aes(age)) + geom_histogram(fill = "blue", color = "black", bins = 20)
```



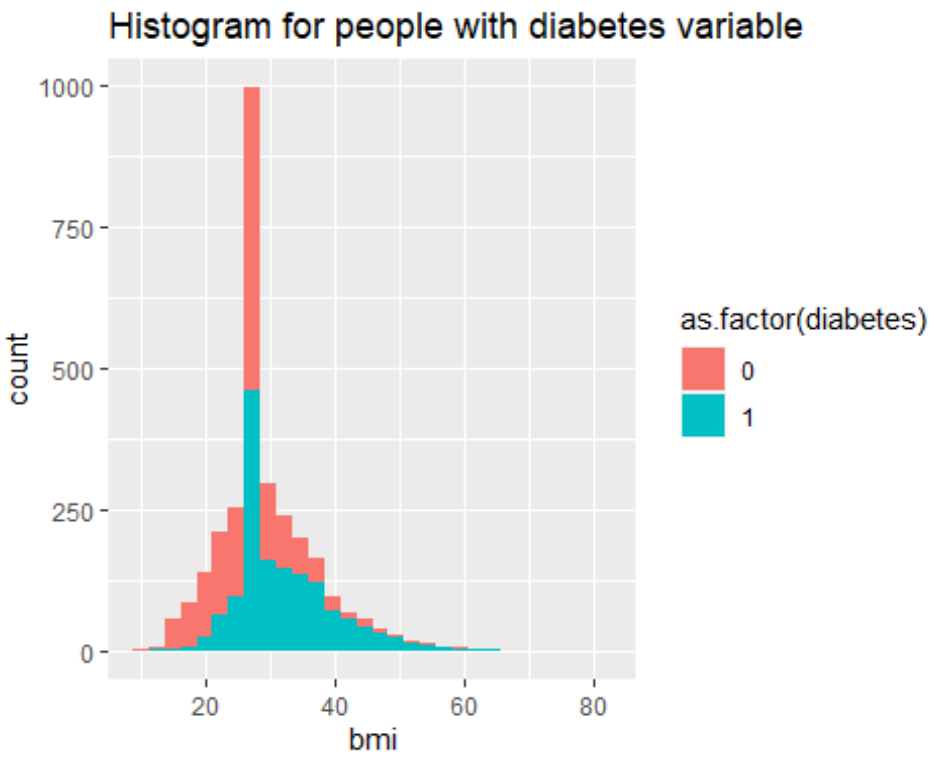

```
#Visualizing the data for age with people whether having diabetes or not
ggplot(diabetesData, aes(x = age, fill = as.factor(diabetes))) + geom_histogram() + labs(title =
"Histogram for people with diabetes variable")

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



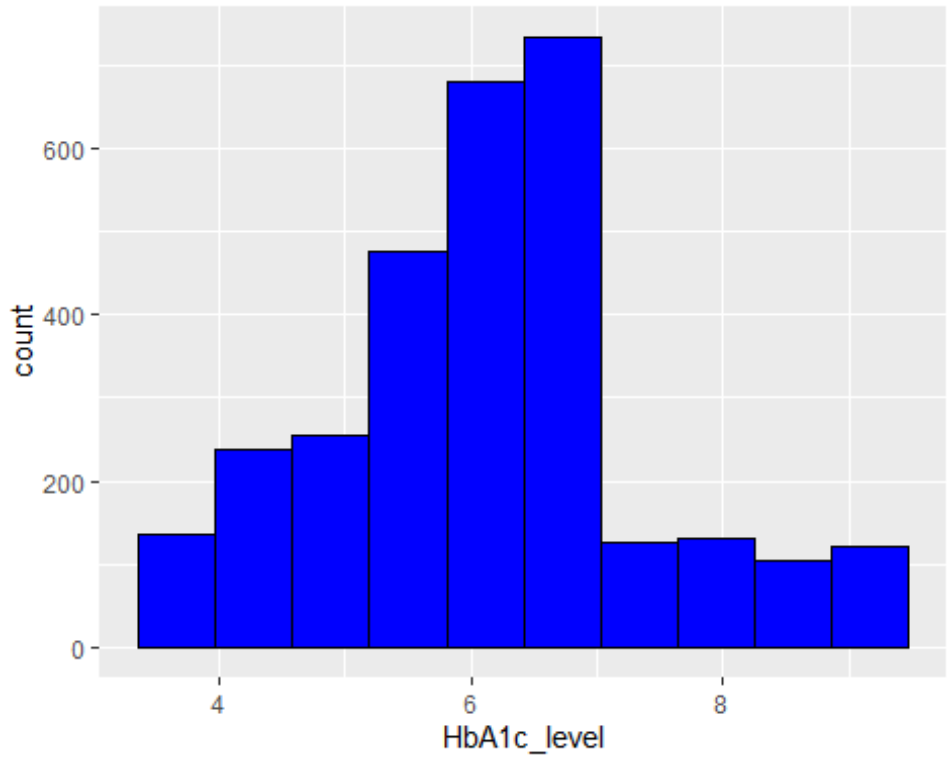

```
#Visualizing the data for variable bmi i.e. body mass index
summary(diabetesData$bmi)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   10.01   25.81   27.32   29.51   33.00   81.73

ggplot(diabetesData, aes(bmi)) + geom_histogram(fill = "blue", color = "black", bins = 20)
```



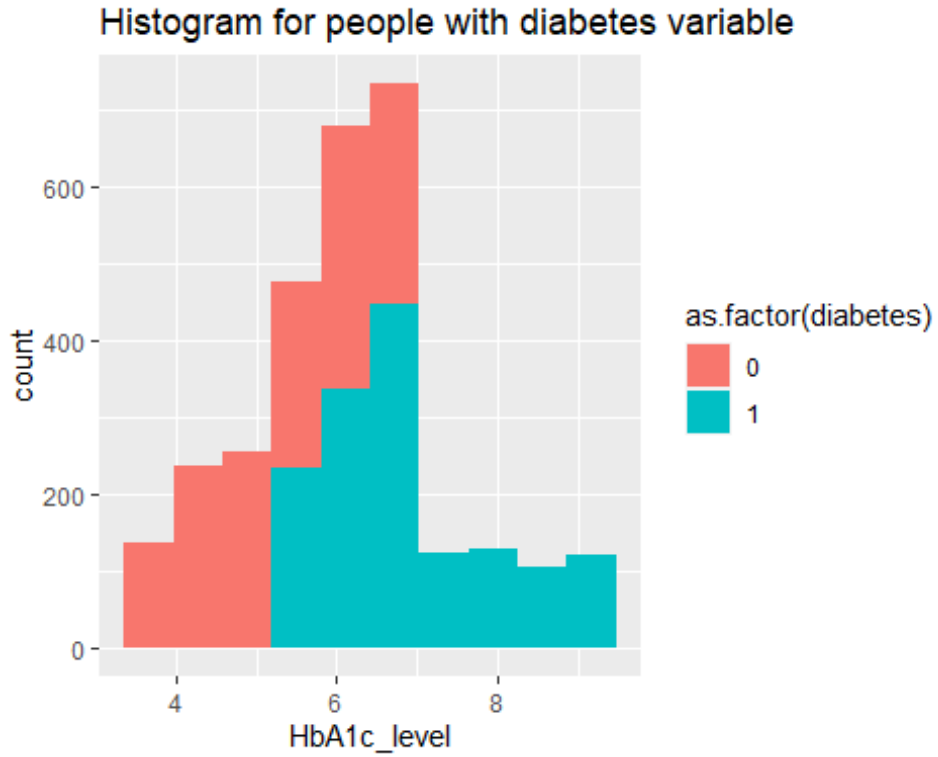

```
#Visualizing the data for age with people whether having diabetes or not
ggplot(diabetesData, aes(x = bmi, fill = as.factor(diabetes))) + geom_histogram() + labs(title =
"Histogram for people with diabetes variable")

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
#Visualizing the data for variable HbA1c_level i.e. hemoglobin level
summary(diabetesData$HbA1c_level)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   3.500   5.700   6.100   6.177   6.600   9.000

ggplot(diabetesData, aes(HbA1c_level)) + geom_histogram(fill = "blue", color = "black", bins = 10)
```



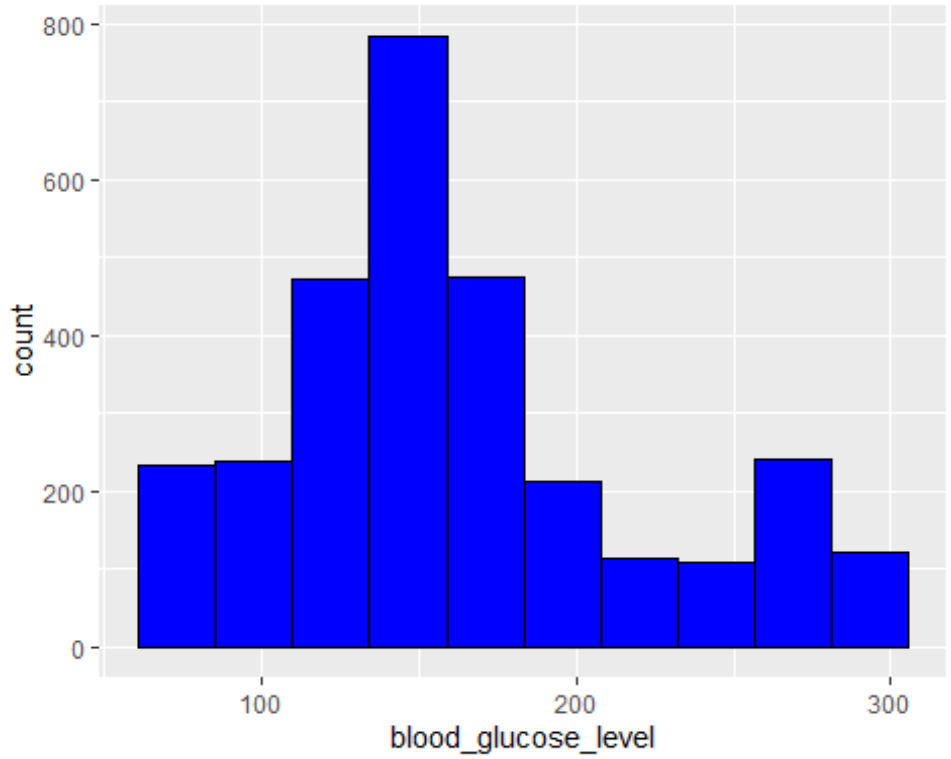

```
#Visualizing the data for age with people whether having diabetes or not
ggplot(diabetesData, aes(x = HbA1c_level, fill = as.factor(diabetes))) + geom_histogram(bins = 10) +
labs(title = "Histogram for people with diabetes variable")
```



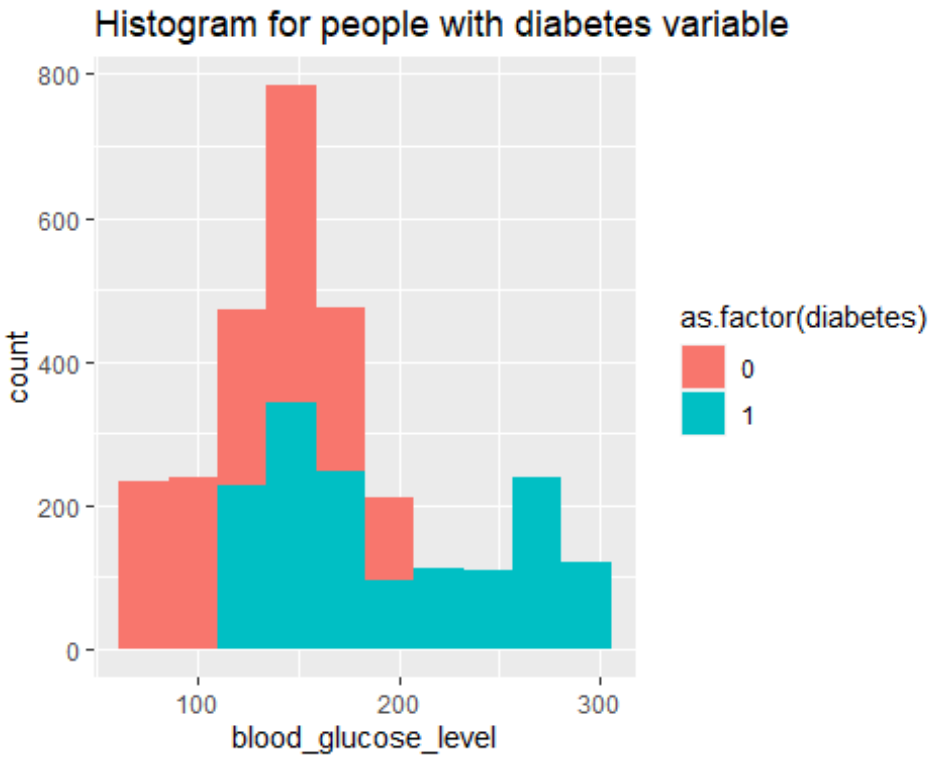
```r
#Visualizing the data for variable blood_glucose_level
summary(diabetesData$blood_glucose_level)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    80.0   130.0   155.0   163.1   200.0   300.0
```

```r
ggplot(diabetesData, aes(blood_glucose_level)) + geom_histogram(fill = "blue", color = "black", bins = 10)
```




```r
#Visualizing the data for age with people whether having diabetes or not
ggplot(diabetesData, aes(x = blood_glucose_level, fill = as.factor(diabetes))) + geom_histogram(bins = 10) + labs(title = "Histogram for people with diabetes variable")
```



There is no need to do barplot for diabetes as there is a data of 1500 observation each.

c. Data Cleaning

Don't forget – this can take a lot of the time of the whole process. Your cleaning process must ensure that there are no missing values and all outliers must be considered. It may be reasonable to just remove rows with missing values, however, if your data or small or that would change the distributions of the variables, that will not be adequate and you will need to consider other options, as discussed in the modules on cleaning.

The dataset as a variable called smoking_history which as a value called no info so as it is not needed for the analysis I am converting those values to NA

```
diabetesData$smoking_history <- ifelse(diabetesData$smoking_history == "No Info", NA,
diabetesData$smoking_history)
head(diabetesData)
```

```
##       gender age hypertension heart_disease smoking_history   bmi HbA1c_level
## 99151 Female  66           0             0          never 36.62        6.6
## 42865 Female  79           1             0          never 29.05        6.8
## 2691  Female  32           0             0          <NA> 30.86         6.5
## 69981 Female  51           0             0          never 27.32        4.0
## 96893 Female  14           0             0           <NA> 18.43         6.5
## 83729 Female  60           0             0          never 25.50        6.1
##       blood_glucose_level diabetes
## 99151                 155        1
## 42865                 155        1
```

```
## 2691               100       0
## 69981               90       0
## 96893              159       1
## 83729               90       0
```

```
summary(diabetesDataSet)
```

```
##    gender              age        hypertension     heart_disease
##  Length:100000      Min.   : 0.08   Min.   :0.00000   Min.   :0.00000
##  Class :character   1st Qu.:24.00   1st Qu.:0.00000   1st Qu.:0.00000
##  Mode  :character   Median :43.00   Median :0.00000   Median :0.00000
##                     Mean   :41.89   Mean   :0.07485   Mean   :0.03942
##                     3rd Qu.:60.00   3rd Qu.:0.00000   3rd Qu.:0.00000
##                     Max.   :80.00   Max.   :1.00000   Max.   :1.00000
##  smoking_history        bmi         HbA1c_level    blood_glucose_level
##  Length:100000      Min.   :10.01   Min.   :3.500   Min.   : 80.0
##  Class :character   1st Qu.:23.63   1st Qu.:4.800   1st Qu.:100.0
##  Mode  :character   Median :27.32   Median :5.800   Median :140.0
##                     Mean   :27.32   Mean   :5.528   Mean   :138.1
##                     3rd Qu.:29.58   3rd Qu.:6.200   3rd Qu.:159.0
##                     Max.   :95.69   Max.   :9.000   Max.   :300.0
##    diabetes
##  Min.   :0.000
##  1st Qu.:0.000
##  Median :0.000
##  Mean   :0.085
##  3rd Qu.:0.000
##  Max.   :1.000
```

As it can be seen in the head the values which are converted to NA are present.

```
#Removing null variables
sum(is.na(diabetesData))
```

```
## [1] 836
```

```
diabetesData <- na.omit(diabetesData)
sum(is.na(diabetesData))
```

```
## [1] 0
```

```
dim(diabetesData)
```

```
## [1] 2164    9
```

```
summary(diabetesData)
```

```
##    gender              age        hypertension    heart_disease
##  Length:2164        Min.   : 0.72   Min.   :0.0000   Min.   :0.0000
##  Class :character   1st Qu.:41.00   1st Qu.:0.0000   1st Qu.:0.0000
##  Mode  :character   Median :57.00   Median :0.0000   Median :0.0000
##                     Mean   :54.08   Mean   :0.1895   Mean   :0.1026
##                     3rd Qu.:69.00   3rd Qu.:0.0000   3rd Qu.:0.0000
```

```
##                 Max.   :80.00   Max.   :1.0000   Max.   :1.0000
##  smoking_history       bmi        HbA1c_level    blood_glucose_level
##  Length:2164       Min.   :11.95   Min.   :3.500   Min.   : 80
##  Class :character   1st Qu.:26.25   1st Qu.:5.700   1st Qu.:130
##  Mode  :character   Median :28.05   Median :6.200   Median :155
##                 Mean   :30.50   Mean   :6.267   Mean   :167
##                 3rd Qu.:34.31   3rd Qu.:6.800   3rd Qu.:200
##                 Max.   :81.73   Max.   :9.000   Max.   :300
##    diabetes
##  Min.   :0.0000
##  1st Qu.:0.0000
##  Median :1.0000
##  Mean   :0.5689
##  3rd Qu.:1.0000
##  Max.   :1.0000
```

As per the data set now we have the clean data, can able to proceed with Data preprocessing.

d. Data Preprocessing

In some cases, preprocessing is absolutely necessary. It is rarely a bad idea. Make the case for what is and is not necessary given what you plan to do with the data. This could include making dummy variables, applying normalization, binning and/or smoothing, and other transformations (see course module).

```
#Creating dummy variables for smoking_history and gender variable
diabetesData$diabetes <- as.factor(diabetesData$diabetes)
diabetesData$gender <- as.factor(diabetesData$gender)
diabetesData$smoking_history <- as.factor(diabetesData$smoking_history)
diabetesData<- cbind(diabetesData,model.matrix(~ gender -1, data = diabetesData))
diabetesData<- cbind(diabetesData,model.matrix(~ smoking_history -1, data = diabetesData))
head(diabetesData)

##       gender age hypertension heart_disease smoking_history   bmi HbA1c_level
## 99151 Female  66           0             0          never 36.62         6.6
## 42865 Female  79           1             0          never 29.05         6.8
## 69981 Female  51           0             0          never 27.32         4.0
## 83729 Female  60           0             0          never 25.50         6.1
## 47091   Male  58           0             0        current 37.65         6.1
## 96663 Female  31           0             0          never 35.80         6.6
##       blood_glucose_level diabetes genderFemale genderMale
## 99151                 155        1            1          0
## 42865                 155        1            1          0
## 69981                  90        0            1          0
## 83729                  90        0            1          0
## 47091                 145        0            0          1
## 96663                  80        0            1          0
##       smoking_historycurrent smoking_historyever smoking_historyformer
## 99151                      0                   0                     0
## 42865                      0                   0                     0
## 69981                      0                   0                     0
```

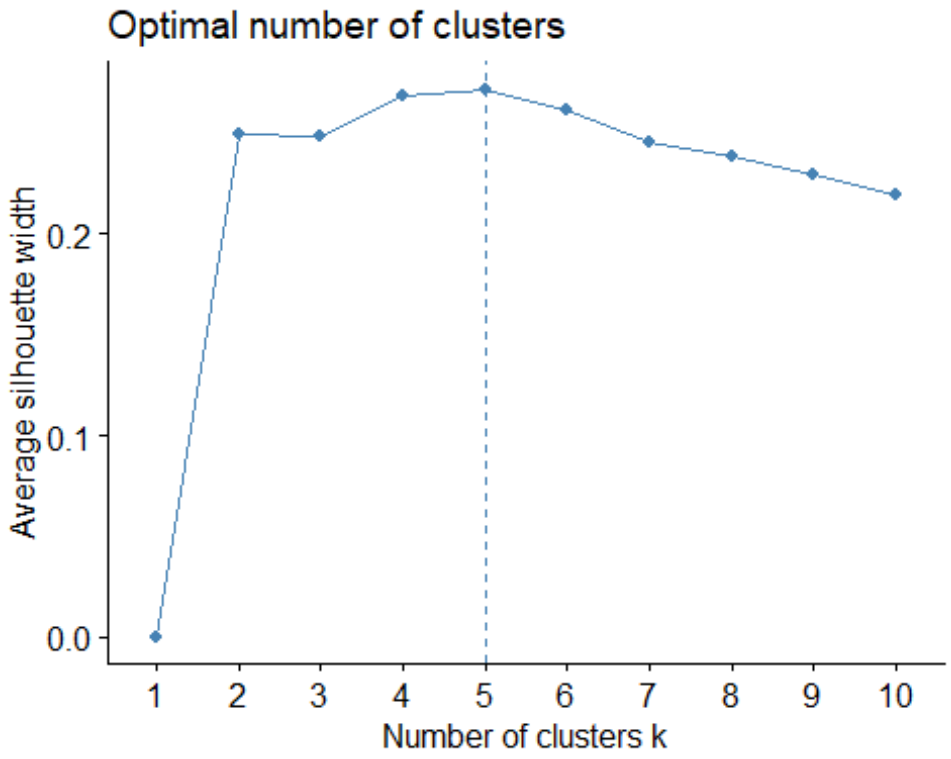
```
## 83729                 0              0              0
## 47091                 1              0              0
## 96663                 0              0              0
##       smoking_historynever smoking_historynot current
## 99151                    1                         0
## 42865                    1                         0
## 69981                    1                         0
## 83729                    1                         0
## 47091                    0                         0
## 96663                    1                         0
```

As normalization or any other types of transformation or not required for the data set because as it is medical data the values needs to actual and doing binning or smoothing can't be done on the data.

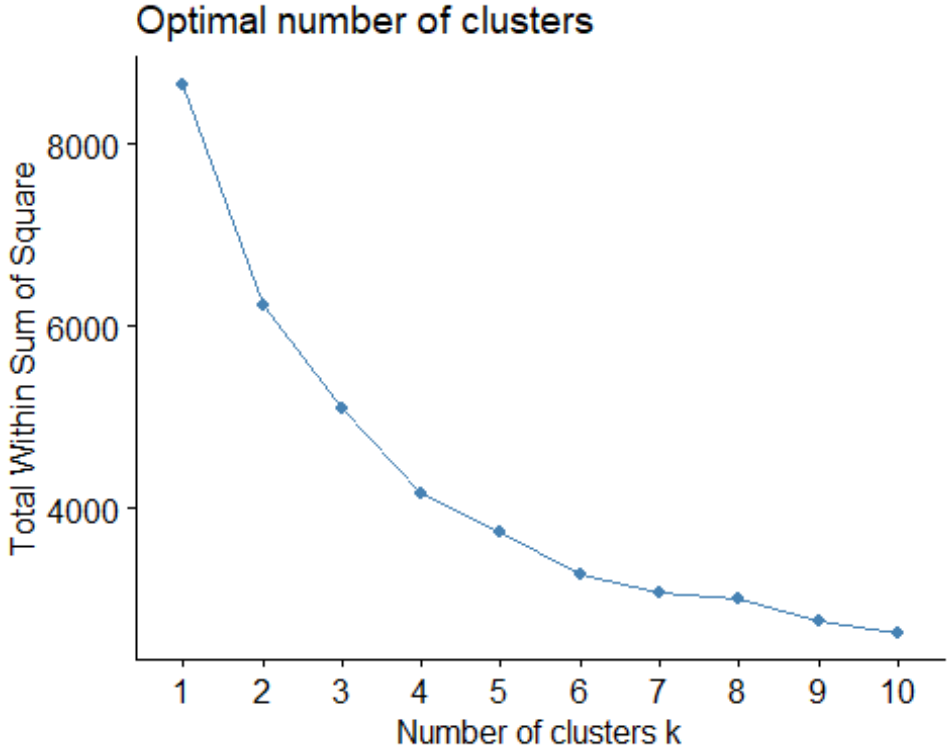
d. Clustering

Remove any labels from your data and use clustering to discover any built-in structure. Use an appropriate method to determine the number of clusters. If our data have labels, compare the clusters to those labels. If not, visualize the clustering results by making a PCA projection and coloring the points by cluster assignment. Note that PCA only works for numerical variables, so if your data have just a few categoricals, you may skip them. If there are many, use dummy variables or choose a different method for making a projection. One way is to make the distance matrix first (we covered a method for distance matrices using categorical variables in the clustering tutorial) and then apply PCA to that matrix. This is actually a way to calculate an MDS projection, a very popular method.

```
fviz_nbclust(predict(preProcess(diabetesData[,c(2, 6, 7, 8)], method = c("center", "scale")),
diabetesData[,c(2, 6, 7, 8)]),
kmeans, method = "silhouette")
```

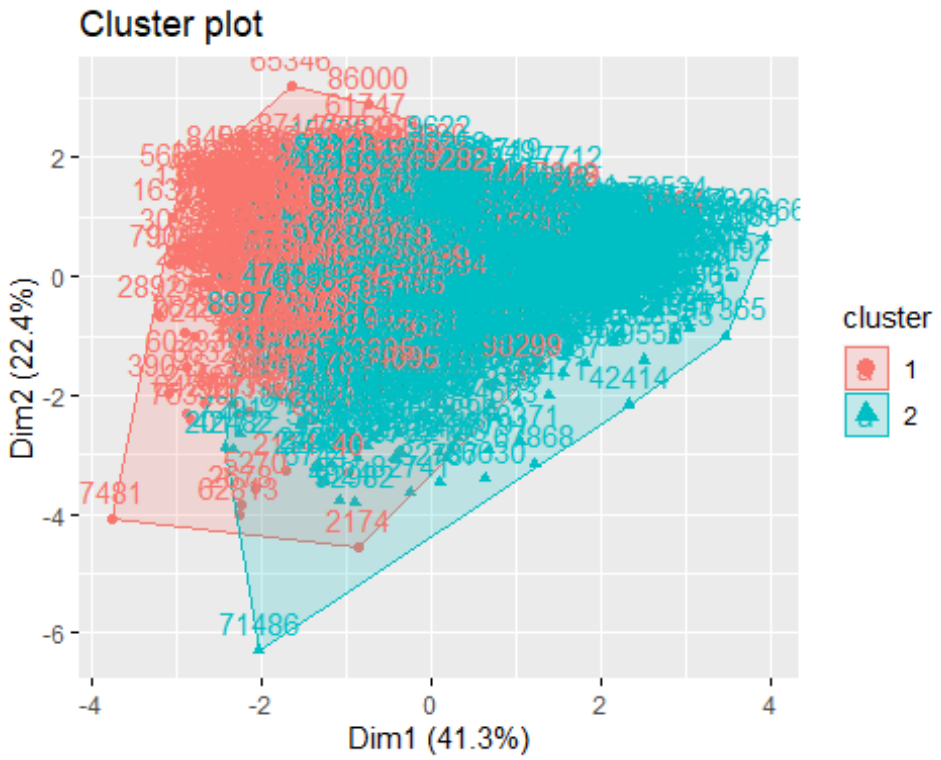



```
fviz_nbclust(predict(preProcess(diabetesData[,c(2, 6, 7, 8)], method = c("center", "scale")),
diabetesData[,c(2, 6, 7, 8)]),
kmeans, method = "wss")
```

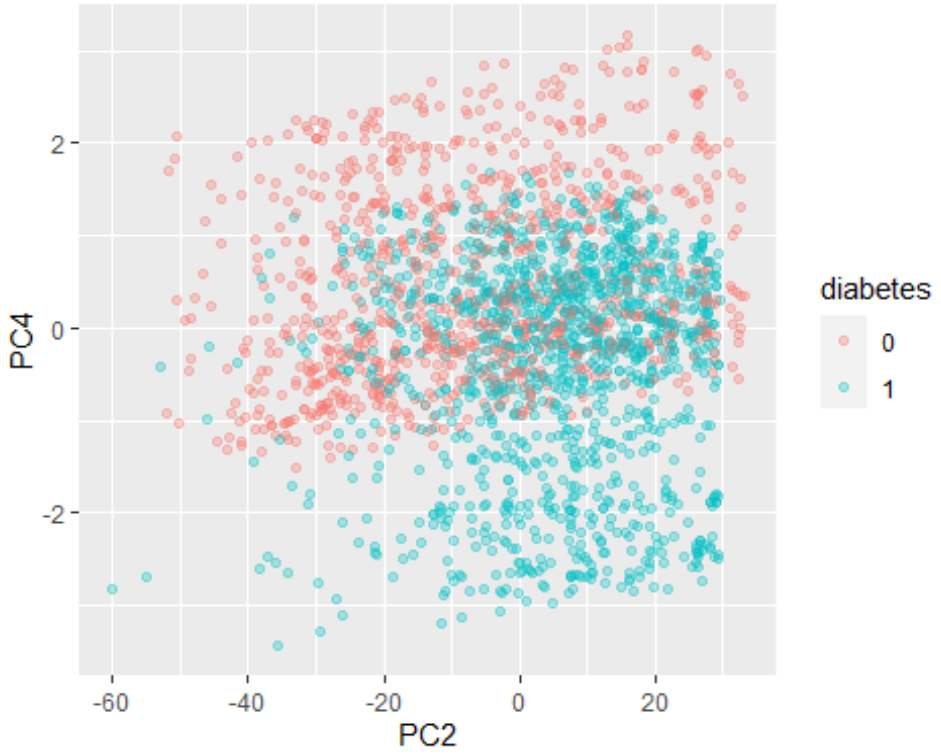


I am choosing the kneel method to make clusters by that plot k value is 2 as the slight l shape is at 2.

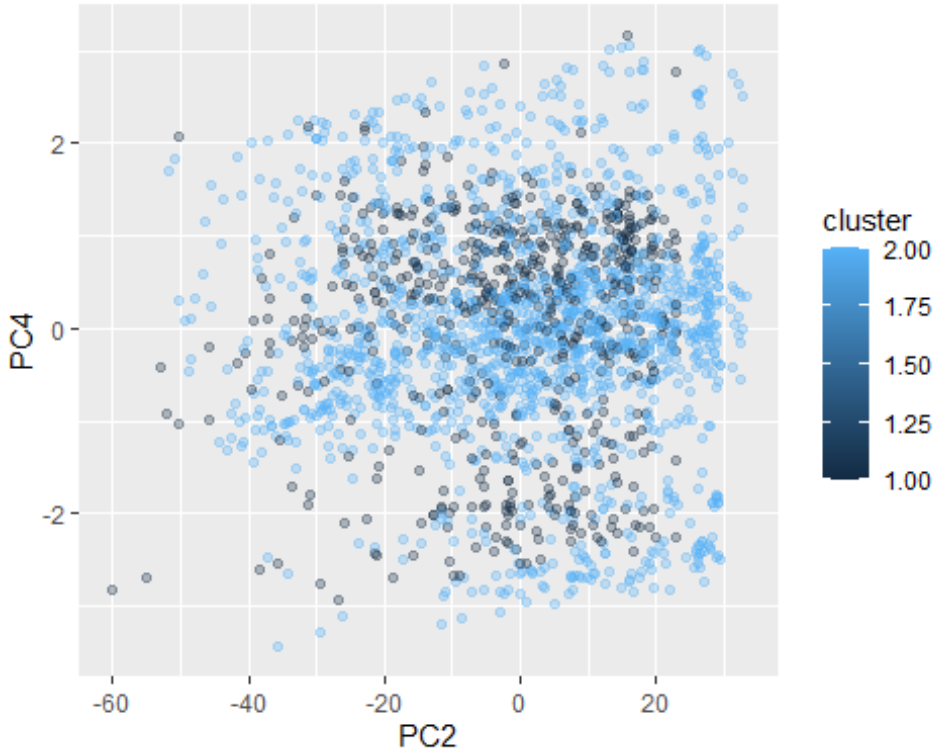
```
kMeansFit <- kmeans(diabetesData[,c(2, 6, 7, 8)], centers = 2, nstart = 25)

fviz_cluster(kMeansFit, data = diabetesData[,c(2, 6, 7, 8)])
```




```
pcaDiabetesNumerical <- prcomp(diabetesData[,c(2, 6, 7, 8)])
pcaRotatedDataNumerical <- as.data.frame(pcaDiabetesNumerical$x)
pcaRotatedDataNumerical$diabetes <- diabetesData$diabetes
ggplot(data = pcaRotatedDataNumerical, aes(x = PC2, y = PC4, col = diabetes)) + geom_point(alpha = 0.3)
```




```
pcaRotatedDataNumerical$cluster <- kMeansFit$cluster
ggplot(data = pcaRotatedDataNumerical, aes(x = PC2, y = PC4, col = cluster)) + geom_point(alpha = 0.3)
```



As comparing two clusters as per the plot the predicted cluster and actual labels are not same. The clustered model is not good.

f. Classification

Use at least two classifiers to predict a label in your data. If a label was not provided with the data, use the clustering from the previous part. Follow the process for choosing the best parameters for your choice of classifier. Compare the accuracy of the two.

As I have labels for the data I am not using k means clustering.

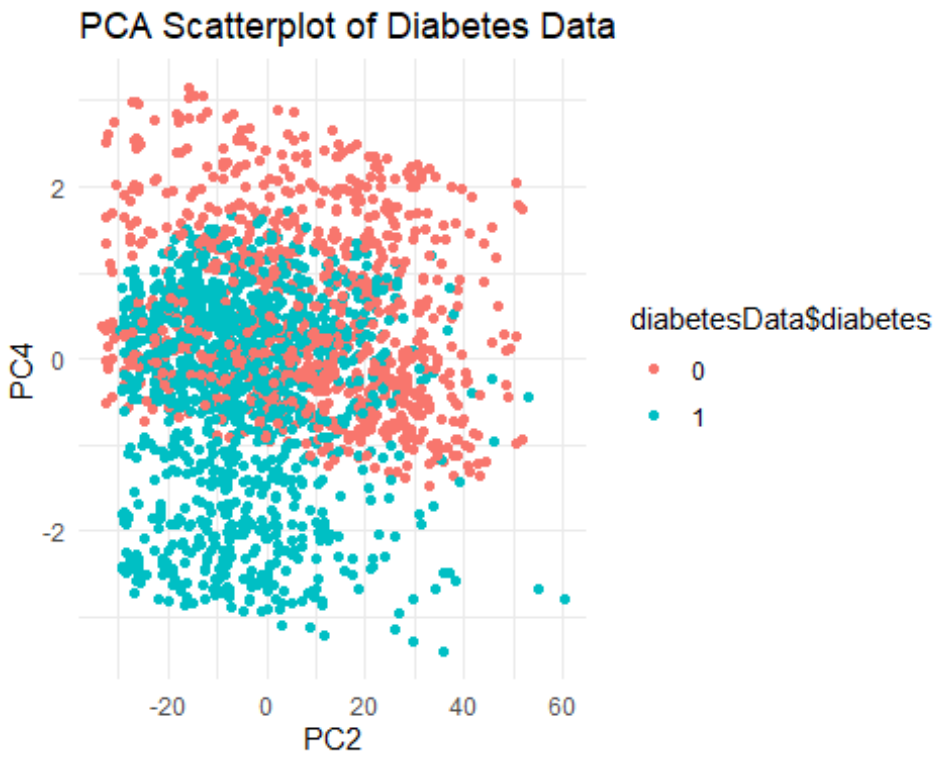
```
#Doing PCA for numerical values
diabetesPCAData <- prcomp(diabetesData[,-c(1,5,9)])
str(diabetesPCAData)
```

```
## List of 5
##  $ sdev    : num [1:13] 58.27 18.18 7.6 1.21 0.71 ...
##  $ rotation: num [1:13, 1:13] -0.08419 -0.000805 -0.00049 -0.021445 -0.007236 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:13] "age" "hypertension" "heart_disease" "bmi" ...
##   .. ..$ : chr [1:13] "PC1" "PC2" "PC3" "PC4" ...
##  $ center  : Named num [1:13] 54.079 0.189 0.103 30.495 6.267 ...
##   ..- attr(*, "names")= chr [1:13] "age" "hypertension" "heart_disease" "bmi" ...
##  $ scale   : logi FALSE
##  $ x       : num [1:2164, 1:13] 10.79 9.86 77.03 76.29 21.41 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:2164] "99151" "42865" "69981" "83729" ...
##   .. ..$ : chr [1:13] "PC1" "PC2" "PC3" "PC4" ...
##  - attr(*, "class")= chr "prcomp"
```

```
summary(diabetesPCAData)
```

```
## Importance of components:
##                           PC1     PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     58.2702 18.1814 7.60012 1.20666 0.71034 0.54868 0.39438
## Proportion of Variance  0.8967  0.0873 0.01525 0.00038 0.00013 0.00008 0.00004
## Cumulative Proportion   0.8967  0.9840 0.99925 0.99964 0.99977 0.99985 0.99989
##                           PC8     PC9    PC10    PC11     PC12      PC13
## Standard deviation     0.37405 0.33044 0.29570 0.27181 7.03e-16 5.067e-16
## Proportion of Variance 0.00004 0.00003 0.00002 0.00002 0.00e+00 0.000e+00
## Cumulative Proportion  0.99993 0.99996 0.99998 1.00000 1.00e+00 1.000e+00
```

```
ggplot(data = as.data.frame(diabetesPCAData$x), aes(x = PC2, y = PC4, color =
diabetesData$diabetes)) +
 geom_point() +
 labs(title = "PCA Scatterplot of Diabetes Data") +
 theme_minimal()
```



As per this plot I will use knn for classification, choosing it might be best as per the plot.

```
diabetesKnn <- train(
 diabetes ~ .,
 data = diabetesData[,-c(1, 5)],
 method = "knn",
 trControl = trainControl(method = "cv", number = 10),
 preProcess = c("center", "scale"),
 tuneLength = 15
)
diabetesKnn
```

```
## k-Nearest Neighbors
##
## 2164 samples
##   13 predictor
##    2 classes: '0', '1'
##
## Pre-processing: centered (13), scaled (13)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 1947, 1948, 1948, 1948, 1948, 1947, ...
## Resampling results across tuning parameters:
##
##   k   Accuracy   Kappa
##    5  0.8521271  0.6960005
##    7  0.8548920  0.7016656
##    9  0.8581221  0.7080488
```

```
##   11  0.8558052  0.7034652
##   13  0.8525708  0.6963847
##   15  0.8581413  0.7084586
##   17  0.8595195  0.7114273
##   19  0.8609127  0.7147531
##   21  0.8572133  0.7075301
##   23  0.8585915  0.7105699
##   25  0.8585936  0.7106808
##   27  0.8576741  0.7086214
##   29  0.8544376  0.7020813
##   31  0.8544398  0.7019439
##   33  0.8558222  0.7051493
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 19.
```

```
#doing classification using svm
diabetesSvm <-  train(
 diabetes ~ .,
 data = diabetesData[,-c(1,5)],
 method = "svmLinear",
 trControl = trainControl(method = "cv", number = 10)
 )
diabetesSvm
```

```
## Support Vector Machines with Linear Kernel
##
## 2164 samples
##   13 predictor
##    2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 1946, 1948, 1948, 1948, 1948, 1948, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.8900233  0.775902
##
## Tuning parameter 'C' was held constant at a value of 1
```

As per the classifications done using knn and svm. The svm has highest accuracy of 89% and other two has accuracy of 86% for knn.

f. Evaluation

Using the better classifier from the previous step, perform a more sophisticated evaluation using the tools of Week 9. Specifically, (1) produce a 2x2 confusion matrix (if your data set has more than two classes, bin the classes into two groups and rebuild the model), (2) calculate the precision and recall manually, and finally (3) produce an ROC plot (see Tutorial 9). Explain how these performance measures makes your classifier look compared to accuracy.

```r
#creating a test data from the existing dataset
partition <- sample(2, nrow(diabetesDataSet), replace = TRUE, prob = c(0.80,0.20))
testData <- diabetesDataSet[partition == 2,]
dim(testData)
```

```
## [1] 19973     9
```

```r
testData$diabetes <- as.factor(testData$diabetes)
testData$gender <- as.factor(testData$gender)
testData$smoking_history <- as.factor(testData$smoking_history)
testData<- cbind(testData,model.matrix(~ gender -1, data = testData))
testData<- cbind(testData,model.matrix(~ smoking_history -1, data = testData))
predictedDiabetesSvm <- predict(diabetesSvm, testData)
diabetesConfusionMatrix <- confusionMatrix(testData$diabetes, predictedDiabetesSvm)
diabetesConfusionMatrix
```

```
## Confusion Matrix and Statistics
##
##          Reference
## Prediction     0     1
##          0 15999  2208
##          1   199  1567
##
##                Accuracy : 0.8795
##                  95% CI : (0.8749, 0.884)
##     No Information Rate : 0.811
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5061
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.9877
##             Specificity : 0.4151
##          Pos Pred Value : 0.8787
##          Neg Pred Value : 0.8873
##              Prevalence : 0.8110
##          Detection Rate : 0.8010
##    Detection Prevalence : 0.9116
##       Balanced Accuracy : 0.7014
##
##       'Positive' Class : 0
##
```

```r
#Confusion matrix for knn
predictedDiabetesKnn <- predict(diabetesKnn, testData)
diabetesConfusionMatrix <- confusionMatrix(testData$diabetes, predictedDiabetesKnn)
diabetesConfusionMatrix
```

```
## Confusion Matrix and Statistics
##
##          Reference
```

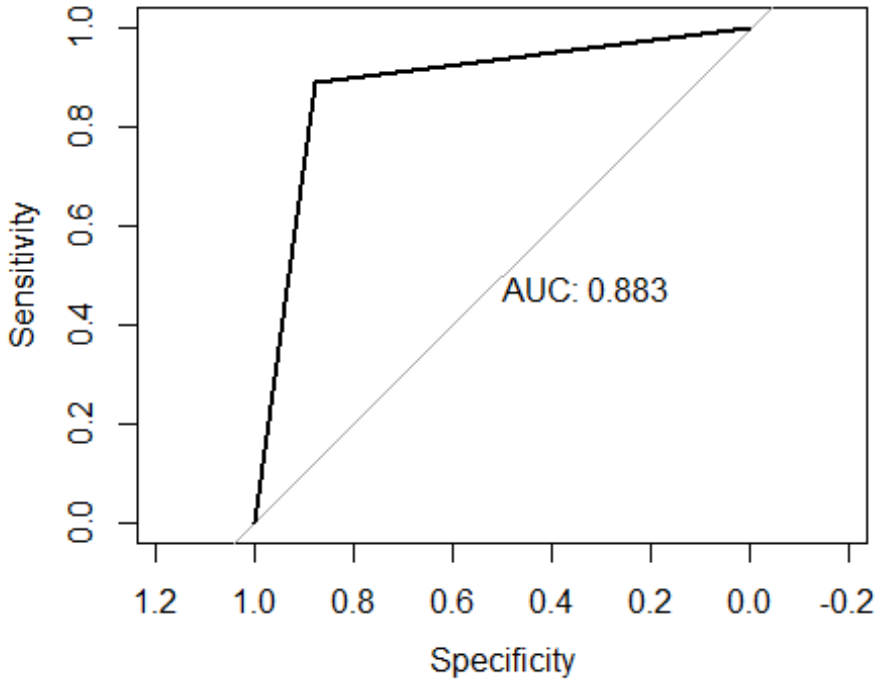
```
## Prediction     0     1
##          0 15041  3166
##          1   210  1556
##
##                Accuracy : 0.831
##                  95% CI : (0.8257, 0.8361)
##     No Information Rate : 0.7636
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.4028
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.9862
##             Specificity : 0.3295
##          Pos Pred Value : 0.8261
##          Neg Pred Value : 0.8811
##              Prevalence : 0.7636
##          Detection Rate : 0.7531
##    Detection Prevalence : 0.9116
##       Balanced Accuracy : 0.6579
##
##        'Positive' Class : 0
##
```

```
roccurve<-roc(response=testData$diabetes, predictor=as.numeric(predictedDiabetesSvm))
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```
plot(roccurve, print.auc=TRUE)
```



In this case, the SVM model would be preferred if we wanted a more balanced classifier because it has a greater AUC and balanced accuracy score. Given how little the overall accuracy scores differ, we could conclude that they are rather close. As can be seen from the confusion matrices, the SVM classifier is actually more accurate at predicting the non-dominant class (positives).

h. Report

After executing the classification methods, I found that the knn is not as accurate as the svm classifier. The reason SVMs were somewhat superior than the decision tree algorithm was because they performed well with generalized data. Furthermore, the kappa number is nearly accurate, suggesting that the data has broader applicability. Due to the two classifiers' extremely high sensitivity, the outcome will not change over time or with successive runs.

i. Reflection

This course has offered insightful information on a variety of data analysis methods, highlighting the need of comprehending different kinds of datasets, data mining, and data visualization. It emphasizes how crucial preprocessing procedures are, including various cleaning approaches and the use of a variety of methods including binning, smoothing, and normalizing to properly handle missing information. Furthermore, the course explores Predictive Machine Learning, emphasizing the comparison of label values with known data using various "classification" techniques, utilizing SVM, Decision Trees, and KNN parameters. Additionally, mastery of "clustering" was attained, employing k-means models and other techniques to predict label values that are unknown. The course also covered discrimination and class differences in more sophisticated assessment using metrics such as recall, accuracy, and ROC along with information about a model's error rate, proving significant beneficial.